

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/561,005
Source: IFWP
Date Processed by STIC: 12/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/561,005

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 _____ Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 _____ Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 _____ Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 _____ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 _____ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 _____ Skipped Sequences
 (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 _____ Skipped Sequences
 (NEW RULES) Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 _____ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 _____ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

- 11 _____ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 _____ PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 _____ Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

RAW SEQUENCE LISTING

DATE: 12/30/2005

PATENT APPLICATION: US/10/561,005

TIME: 09:45:20

Input Set : A:\103-PCT1-US1.ST25.txt

Output Set: N:\CRF4\12302005\J561005.raw

3 <110> APPLICANT: Paz Einat et al./Quark Biotech, Inc.
 5 <120> TITLE OF INVENTION: Methods for cloning nucleic acids in a desired orientation
 7 <130> FILE REFERENCE: 103/PCT1-US1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/561,005
 C--> 10 <141> CURRENT FILING DATE: 2005-12-16
 12 <150> PRIOR APPLICATION NUMBER: PCT/IL 2004/000515
 13 <151> PRIOR FILING DATE: 2004-06-15
 15 <150> PRIOR APPLICATION NUMBER: 60/479,224
 16 <151> PRIOR FILING DATE: 2003-06-16
 18 <160> NUMBER OF SEQ ID NOS: 14
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 24
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Artificial DNA
 31 <220> FEATURE:
 32 <221> NAME/KEY: misc_feature
 33 <222> LOCATION: (21)..(24)
 34 <223> OTHER INFORMATION: "n"=nucleotide A, T, G or C
 36 <400> SEQUENCE: 1
 W-OK 37 gccattaagg ccaccatgcc nnnn 24
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 41
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Artificial
 45 <220> FEATURE:
 46 <223> OTHER INFORMATION: Artificial DNA
 48 <400> SEQUENCE: 2
 49 catggtggcc ttaatggcca ctacgaccgt tcgggtgga c 41
 52 <210> SEQ ID NO: 3
 53 <211> LENGTH: 24
 54 <212> TYPE: DNA
 55 <213> ORGANISM: Artificial
 57 <220> FEATURE:
 58 <223> OTHER INFORMATION: Artificial DNA
 61 <220> FEATURE:
 62 <221> NAME/KEY: misc_feature
 63 <222> LOCATION: (21)..(24)
 64 <223> OTHER INFORMATION: n=nucleotide A, T, G or C
 66 <400> SEQUENCE: 3
 OK 67 gccattaagg ccaccatgcc nnnn 24

ppr 1-4
 Does Not Comply
 Corrected Diskette Needed

insufficient explanation

(give source of genetic material)

(see item 11 on Euro
 summary
 sheet)

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Input Set : A:\103-PCT1-US1.ST25.txt

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70 <210> SEQ ID NO: 4
 71 <211> LENGTH: 41
 72 <212> TYPE: DNA
 73 <213> ORGANISM: Artificial
 75 <220> FEATURE:
 76 <223> OTHER INFORMATION: Artificial DNA
 78 <400> SEQUENCE: 4
 79 catggtgggc ttgccagcat caccggaat tccggtggta c 41
 82 <210> SEQ ID NO: 5
 83 <211> LENGTH: 21
 84 <212> TYPE: DNA
 85 <213> ORGANISM: Artificial
 87 <220> FEATURE:
 88 <223> OTHER INFORMATION: Artificial DNA
 91 <220> FEATURE:
 92 <221> NAME/KEY: misc_feature
 93 <222> LOCATION: (1)..(4)
 94 <223> OTHER INFORMATION: n = nucleotide A, T, G or C
 96 <400> SEQUENCE: 5
 97 nnnnggtgag tgactgaggc c 21
 100 <210> SEQ ID NO: 6
 101 <211> LENGTH: 44
 102 <212> TYPE: DNA
 103 <213> ORGANISM: Artificial
 105 <220> FEATURE:
 106 <223> OTHER INFORMATION: Artificial DNA
 108 <400> SEQUENCE: 6
 109 cgaggagcga ccgactcgat ggccgaggcg gcctcagtc a ctca 44
 112 <210> SEQ ID NO: 7
 113 <211> LENGTH: 21
 114 <212> TYPE: DNA
 115 <213> ORGANISM: Artificial
 117 <220> FEATURE:
 118 <223> OTHER INFORMATION: Artificial DNA
 121 <220> FEATURE:
 122 <221> NAME/KEY: misc_feature
 123 <222> LOCATION: (1)..(4)
 124 <223> OTHER INFORMATION: n = nucleotide A, T, G or C
 126 <400> SEQUENCE: 7
 127 nnnnggtgag tgactgaggc c 21
 130 <210> SEQ ID NO: 8
 131 <211> LENGTH: 44
 132 <212> TYPE: DNA
 133 <213> ORGANISM: Artificial
 135 <220> FEATURE:
 136 <223> OTHER INFORMATION: Artificial DNA
 138 <400> SEQUENCE: 8
 139 actcactgac tccggcggag ccggtagctc agccagcgag gagc 44
 142 <210> SEQ ID NO: 9

RAW SEQUENCE LISTING

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Input Set : A:\103-PCT1-US1.ST25.txt

Output Set: N:\CRF4\12302005\J561005.raw

143 <211> LENGTH: 21
 144 <212> TYPE: DNA
 145 <213> ORGANISM: Artificial
 147 <220> FEATURE:
 148 <223> OTHER INFORMATION: Artificial DNA
 150 <400> SEQUENCE: 9
 151 gtaccacccg aacggtcgta g 21
 154 <210> SEQ ID NO: 10
 155 <211> LENGTH: 13
 156 <212> TYPE: DNA
 157 <213> ORGANISM: Artificial
 159 <220> FEATURE:
 160 <223> OTHER INFORMATION: Artificial DNA
 163 <220> FEATURE:
 164 <221> NAME/KEY: misc_feature
 165 <222> LOCATION: (5)..(9)
 166 <223> OTHER INFORMATION: n = nucleotide A, T, G or C
 168 <400> SEQUENCE: 10
 169 ggccnnnnng gcc 13
 172 <210> SEQ ID NO: 11
 173 <211> LENGTH: 13
 174 <212> TYPE: DNA
 175 <213> ORGANISM: Artificial
 177 <220> FEATURE:
 178 <223> OTHER INFORMATION: Artificial DNA
 181 <220> FEATURE:
 182 <221> NAME/KEY: misc_feature
 183 <222> LOCATION: (5)..(9)
 184 <223> OTHER INFORMATION: n = nucleotide A, T, G or C
 186 <400> SEQUENCE: 11
 187 ccggnnnnnc cgg 13
 190 <210> SEQ ID NO: 12
 191 <211> LENGTH: 5
 192 <212> TYPE: DNA
 193 <213> ORGANISM: Artificial
 195 <220> FEATURE:
 196 <223> OTHER INFORMATION: Artificial DNA
 198 <400> SEQUENCE: 12
 199 aggcc 5
 202 <210> SEQ ID NO: 13
 203 <211> LENGTH: 5
 204 <212> TYPE: DNA
 205 <213> ORGANISM: Artificial
 207 <220> FEATURE:
 208 <223> OTHER INFORMATION: Artificial DNA
 210 <400> SEQUENCE: 13
 211 ccggg 5
 214 <210> SEQ ID NO: 14
 215 <211> LENGTH: 46

RAW SEQUENCE LISTING

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Input Set : A:\103-PCT1-US1.ST25.txt

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216 <212> TYPE: DNA

217 <213> ORGANISM: Artificial

219 <220> FEATURE:

220 <223> OTHER INFORMATION: Artificial DNA

222 <400> SEQUENCE: 14

223 gaattggcca ttaaggcctg caggatccgg ccgcctcggc ctcgag

46

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 12/30/2005

PATENT APPLICATION: US/10/561,005

TIME: 09:45:21

Input Set : A:\103-PCT1-US1.ST25.txt

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. ~~21,22,23,24~~Seq#:3; N Pos. ~~21,22,23,24~~Seq#:5; N Pos. ~~1,2,3,4~~Seq#:7; N Pos. ~~1,2,3,4~~Seq#:10; N Pos. ~~5,6,7,8,9~~

Seq#:11; N Pos. 5,6,7,8,9

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14

VERIFICATION SUMMARY

DATE: 12/30/2005

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TIME: 09:45:21

Input Set : A:\103-PCT1-US1.ST25.txt

Output Set: N:\CRF4\12302005\J561005.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:67 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:97 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0